

IDENTIFICATION

Species: *Setaria viridis*

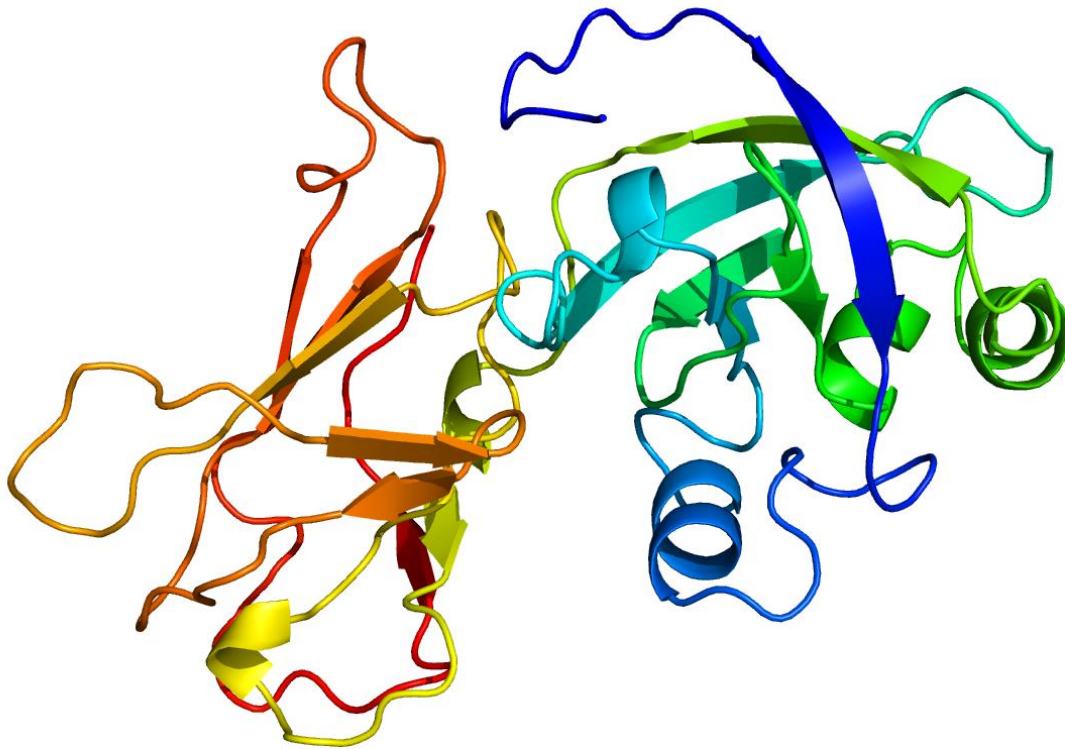
Locus: Sevir.2G333300

Gene Model: Sevir.2G333300.1.p

Description: SvEXLB-01

Family: Expansin Like Beta

3D structure:



GENOME DATABASES

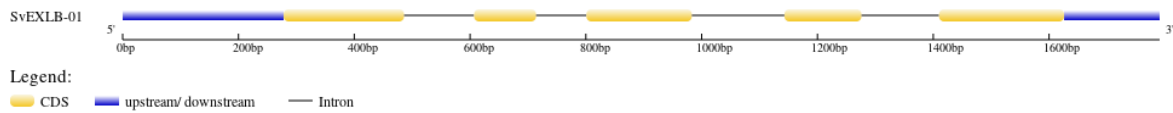
Phytozome: https://phytozome-next.jgi.doe.gov/info/Sviridis_v2_1

KEGG:-

EXTERNAL RESOURCES

-

GENE STRUCTURE



DOMAIN ARCHITECTURE

Query seq. Superfamilies

List of domain hits

Name	Accession	Description	Interval	E-value
PLN03023 super family	cl33621	Expansin-like B1; Provisional	32-278	1.09e-78

SEQUENCES

Peptide

>SvEXLB-01

MTPSLILYICTIQSSKPCSFVSVPMQMAFPMHCLSALLYLFALISKATADANFTVSKAVH
YPNSDTRGTETGACEYGAFGATLNNGDVSASASLYRNGVGCACGYQVRCTNPHYCS
PSGVTIVITDSGASNGTDFILSQHAFAGMGQNKDAGATLLNLGYVGIEYRRVPCIYPG
KNIIFKITESSHPYYLEFEIWIYQQGNQDIIAVQLCETVNLTCQLLGRTHGAVWAAISP
PNGPLNIRMLFSSGAPHRGDQKWLVTSTIPQNWTAGATYDSGVQVQLQ*

CDS (coding sequence)

>SvEXLB-01

ATGACTCCATCTCTCATCTTATATATATGTACAATACAATCTTCTAAGCCTTGTTT
GTTCTGCTCTGTGCCACAGATGGCTTTTCCCATGCACTGCCTCTCAGCTTTGCTTT
ATCTGTTTGCCTCATCTCCAAGGCTACTGCAGATGCAAATTCACGGTGTCAA
AGCAGTACACTACCCAACTCTGATACACGAGGGACCGAACTGGAGCATGTGA
ATATGGTGCATTTGGGGCAACGCTCAACAATGGAGATGTTTCAGCATCAGCAAGT
CTATACAGGAATGGGGTAGGCTGTGGTGCATGCTACCAGGTTAGGTGCACAAATC
CTCACTACTGCTCCCCAAGTGGAGTGACAATCGTGATCACAGACTCTGGGGCAAG
CAACGGGACTGACTTCATCCTGAGCCAGCACGCCTTCGCTGGGATGGGGCAGAAC
AAGGACGCTGGTGCACACTGCTGAACCTTGGTTATGTTGGAATTGAGTACAGGA
GGGTTCCATGTATCTACCCAGGCAAGAATATTATATTCAAGATTACTGAGAGCAG
CCATTTCCCTTACTATCTTGAATTTGAGATATGGTACCAACAAGGCAACCAGGAT
ATTATTGCAGTCCAGCTTTGTGAGACTGTGAACCTGACATGCCAGCTTCTGGGCC
GAACTCATGGTGCAGTATGGGCTGCTATCTCCCCACCAAATGGCCCTCTGAACAT
AAGGATGCTATTTAGCAGCGGAGCTCCACATCGCGGCGACCAGAAATGGCTGGTT
TCCACAAGCACAATACCACAGA ACTGGACAGCAGGAGCCACGTACGATTCTGGG
GTCCAAGTGCAGCTGCAGTAG

Nucleotide

>SvEXLB-01

TATTTATCAGTTGTAAAAGTCAAATTCCAAAACCAA ACTCTCCAGACACGGGAAC
GGAACATTTCTAAAACAATGAGACCCTGGAAACAGAACTTCCAGACAGCGCCTA
CTTCTCGAGAATGAAGAAAGGAATCACAAGGACTCAGGCACGTGTGCACTCAG
AGAAGCATATTCAACAACAGCATTGGCATCCCCATCCATTCAAACCAAAGTTT

CCAGCTCGTAACTCGTGAGCAGCCTAAGGGGAGGCACCTCAAGTTGAGCACTATA
AATACATGACTCCATCTCTCATCTTATATATATGTACAATAACAATCTTCTAAGCCT
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CAAAAGCAGTACACTACCCCAACTCTGATACACGAGGGACCGAAAGTAAGTAAC
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AGCTGGAGCATGTGAATATGGTGCATTTGGGGCAACGCTCAACAATGGAGATGTT
TCAGCATCAGCAAGTCTATACAGGAATGGGGTAGGCTGTGGTGCATGCTACCAGG
TAAATTCATTTCCGCCAGCAGTAGTTGTGTAAACTACGAAACATAACTCCTTTGAT
CAAATAAGATTGTTTGTGACTGCCAACAGGTTAGGTGCACAAATCCTCACTACT
GCTCCCAAGTGGAGTGACAATCGTGATCACAGACTCTGGGGCAAGCAACGGGA
CTGACTTCATCCTGAGCCAGCACGCCTTCGCTGGGATGGGGCAGAACAAGGACGC
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